WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid comprising a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID NO:25, over a region of at least about 100 residues, wherein the nucleic acid encodes at least one polypeptide having a laccase activity, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.

2. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63% or 64%.

3. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID NO:25.

4. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, or the full length of a gene or a transcript.

5. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence comprises a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID NO:25.

6. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence encodes a polypeptide having a sequence as set forth in SEQ ID

NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26.

7. The isolated or recombinant nucleic acid of claim 1, wherein the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

8. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity comprises the depolymerization of lignin.

9. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity comprises the polymerization of lignin.

10. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity comprises catalyzing the oxidation of 1-hydroxybenzotriazole (HBT), N-benzoyl-N-phenyl hydroxylamine (BPHA), N-hydroxyphthalimide, 3-hydroxy-1,2,3-benzotriazin-4-one, promazine, 1,8-dihydroxy-4,5-dinitroanthraquinone, phenoxazine, anthraquinone, 2-hydroxy-1,4-naphthoquinone, phenothiazine, syringaldazine, anthrone, anthracene, anthrarufin, anthrarobin, 2,2'-azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) (ABTS), dimethoxyphenol (DMP), ferulic acid, catechin, epicatechin, homovanillic acid (HMV), 2,3-dihydroxybenzoic acid (2,3-DHB), 2,2,6,6-tetramethylpiperidin-1-yloxy (TEMPO), dimethoxyphenol or dihydroxyfumaric acid (DHF).

11. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity comprises the depolymerization of a cellulose or a cellulose derivative or a hemicellulose.

12. The isolated or recombinant nucleic acid of claim 11, wherein the cellulose derivative comprises a carboxy methyl cellulose or a hydroxy ethyl cellulose.

13. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity comprises production of a nootkatone from a valencene.

14. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity comprises a peroxidase activity.

15. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity comprises oxidation of a cellulose, a cellulose derivative or a hemicellulose.

16. The isolated or recombinant nucleic acid of claim 15, wherein the laccase activity comprises oxidation of a cellulose or a hemicellulose in a wood or paper pulp or a wood or paper product.

17. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity comprises catalyzing the oxidation of a lignin in a feed, a food product or a beverage.

18. The isolated or recombinant nucleic acid of claim 17, wherein the feed, food product or beverage comprises a cereal-based animal feed, a wort or a beer, a dough, a fruit or a vegetable.

19. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity comprises catalyzing the oxidation of a lignin in a microbial cell, a fungal cell, a mammalian cell or a plant cell.

20. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity comprises catalysis of an aromatic substrate.

21. The isolated or recombinant nucleic acid of claim 20, wherein the laccase activity comprises a polyphenol, a methoxy-substituted monophenol, an aromatic amine, or an oxidizable aromatic compound.

22. The isolated or recombinant nucleic acid of claim 1, wherein the laccase activity is thermostable or thermotolerant.

23. The isolated or recombinant nucleic acid of claim 22, wherein the polypeptide retains a laccase activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C, or, the polypeptide retains a laccase activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C.

24. An isolated or recombinant nucleic acid, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a nucleic acid comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID NO:25, wherein the nucleic acid encodes a polypeptide having a laccase activity.

25. The isolated or recombinant nucleic acid of claim 24, wherein the nucleic acid is at least about 50, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript.

26. The isolated or recombinant nucleic acid of claim 24, wherein the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

27. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide with a laccase activity, wherein the probe comprises at least 10 consecutive bases of a sequence comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID NO:25, wherein the probe identifies the nucleic acid by binding or hybridization.

28. The nucleic acid probe of claim 27, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

29. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a laccase activity, wherein the probe comprises a nucleic acid comprising at least about 10 consecutive residues of a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID NO:25, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection.

30. The nucleic acid probe of claim 29, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

31. An amplification primer pair for amplifying a nucleic acid encoding a polypeptide having a laccase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

32. The amplification primer pair of claim 31, wherein a member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.

33. An amplification primer pair, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 42, 33, 34, 35 or more residues of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID NO:25, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 42, 33, 34, 35 or more residues of the complementary strand of the first member.

34. A laccase-encoding nucleic acid generated by amplification of a polynucleotide using an amplification primer pair as set forth in claim 33.

35. The laccase-encoding nucleic acid of claim 34, wherein the amplification is by polymerase chain reaction (PCR).

36. The laccase-encoding nucleic acid of claim 34, wherein the nucleic acid generated by amplification of a gene library.

37. The laccase-encoding nucleic acid of claim 34, wherein the gene library is an environmental library.

38. An isolated or recombinant laccase encoded by a laccase-encoding nucleic acid as set forth in claim 34.

39. A method of amplifying a nucleic acid encoding a polypeptide having a laccase activity comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

40. An expression cassette comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

41. A vector comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

42. A cloning vehicle comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

43. The cloning vehicle of claim 42, wherein the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector.

44. The cloning vehicle of claim 42, comprising a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

45. A transformed cell comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

46. A transformed cell comprising an expression cassette as set forth in claim 40.

47. The transformed cell of claim 40, wherein the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

48. A transgenic non-human animal comprising a sequence as set forth in claim 1 or claim 24.

49. The transgenic non-human animal of claim 48, wherein the animal is a mouse.

50. A transgenic plant comprising a sequence as set forth in claim 1 or claim 24.

51. The transgenic plant of claim 50, wherein the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

52. A transgenic seed comprising a sequence as set forth in claim 1 or claim 24.

53. The transgenic seed of claim 52, wherein the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

54. An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

55. The antisense oligonucleotide of claim 49, wherein the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

56. A method of inhibiting the translation of a laccase message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 24.

57. A double-stranded inhibitory RNA (RNAi) molecule comprising a subsequence of a sequence as set forth in claim 1 or claim 24.

58. The double-stranded inhibitory RNA (RNAi) molecule of claim 52, wherein the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length.

59. A method of inhibiting the expression of a laccase in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of a sequence as set forth in claim 1 or claim 24.

60. An isolated or recombinant polypeptide (i) having at least 50% sequence identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, over a region of at least about 100 residues, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection, or, (ii) encoded by a nucleic acid having at least 50% sequence identity to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID

NO:25, over a region of at least about 100 residues, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection, or encoded by a nucleic acid capable of hybridizing under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID NO:25.

61. The isolated or recombinant polypeptide of claim 60, wherein the sequence identity is over a region of at least about at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or is 100% sequence identity.

62. The isolated or recombinant polypeptide of claim 60, wherein the sequence identity is over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050 or more residues, or the full length of an enzyme.

63. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide has a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 or SEQ ID NO:26.

64. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide has a laccase activity.

65. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises the depolymerization of lignin.

66. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises the polymerization of lignin.

67. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises catalyzing the oxidation of 1-hydroxybenzotriazole (HBT), N-benzoyl-N-phenyl hydroxylamine (BPHA), N-hydroxyphthalimide, 3-hydroxy-1,2,3-benzotriazin-4-one, promazine, 1,8-dihydroxy-4,5-dinitroanthraquinone, phenoxazine, anthraquinone, 2-hydroxy-1,4-naphthoquinone, phenothiazine, syringaldazine, anthrone, anthracene, anthrarufin, anthrarobin, 2,2'-azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) (ABTS), dimethoxyphenol (DMP), ferulic acid, catechin, epicatechin, homovanillic acid (HMV), 2,3-dihydroxybenzoic acid (2,3-DHB), 2,2,6,6-tetramethylpiperidin-1-yloxy (TEMPO), dimethoxyphenol or dihydroxyfumaric acid (DHF).

68. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises the depolymerization of a cellulose or a cellulose derivative or a hemicellulose.

69. The isolated or recombinant polypeptide of claim 68, wherein the cellulose derivative comprises a carboxy methyl cellulose or a hydroxy ethyl cellulose.

70. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises production of a nootkatone from a valencene.

71. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises a peroxidase activity.

72. The isolated or recombinant polypeptide of claim 71, wherein the laccase activity comprises oxidation of a cellulose, a cellulose derivative or a hemicellulose.

73. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises oxidation of a cellulose or a hemicellulose in a wood or paper pulp or a wood or paper product.

74. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises catalyzing the oxidation of a lignin in a feed, a food product or a beverage.

75. The isolated or recombinant polypeptide of claim 74, wherein the feed, food product or beverage comprises a cereal-based animal feed, a wort or a beer, a dough, a fruit or a vegetable.

76. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises catalyzing the oxidation of a lignin in a microbial cell, a fungal cell, a mammalian cell or a plant cell.

77. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises catalysis of an aromatic substrate.

78. The isolated or recombinant polypeptide of claim 77, wherein the laccase activity comprises a polyphenol, a methoxy-substituted monophenol, an aromatic amine, or an oxidizable aromatic compound.

79. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity is thermostable or thermotolerant.

80. The isolated or recombinant polypeptide of claim 77, wherein the polypeptide retains a laccase activity under conditions comprising a temperature range of between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 95°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or, the polypeptide retains a laccase activity after exposure to a temperature in the range from between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more.

81. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 60 and lacking a signal sequence or a prepro sequence.

82. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 60 and having a heterologous signal sequence or a heterologous prepro sequence.

83. The isolated or recombinant polypeptide of claim 64, wherein the laccase activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein.

84. The isolated or recombinant polypeptide of claim 79, wherein the thermotolerance comprises retention of at least half of the specific activity of the laccase at 37°C after being heated to an elevated temperature.

85. The isolated or recombinant polypeptide of claim 79, wherein the thermotolerance comprises retention of specific activity at 37°C in the range from about 500 to about 1200 units per milligram of protein after being heated to an elevated temperature.

86. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises at least one glycosylation site.

87. The isolated or recombinant polypeptide of claim 86, wherein the glycosylation is an N-linked glycosylation.

88. The isolated or recombinant polypeptide of claim 87, wherein the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

89. The isolated or recombinant polypeptide of claim 64, wherein the polypeptide retains a laccase activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0.

90. The isolated or recombinant polypeptide of claim 64, wherein the polypeptide retains a laccase activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5.

91. A protein preparation comprising a polypeptide as set forth in claim 60, wherein the protein preparation comprises a liquid, a solid or a gel.

92. A heterodimer comprising a polypeptide as set forth in claim 60 and a second domain.

93. The heterodimer of claim 92, wherein the second domain is a polypeptide and the heterodimer is a fusion protein.

94. The heterodimer of claim 92, wherein the second domain is an epitope or a tag.

95. A homodimer comprising a polypeptide as set forth in claim 60.

96. An immobilized polypeptide, wherein the polypeptide comprises a sequence as set forth in claim 60, or a subsequence thereof.

97. The immobilized polypeptide of claim 96, wherein the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

98. An array comprising an immobilized polypeptide as set forth in claim 60.

99. An array comprising an immobilized nucleic acid as set forth in claim 1 or claim 24.

100. An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 60.

101. The isolated or recombinant antibody of claim 100, wherein the antibody is a monoclonal or a polyclonal antibody.

102. A hybridoma comprising an antibody that specifically binds to a polypeptide as set forth in claim 60.

103. A method of isolating or identifying a polypeptide with a laccase activity comprising the steps of:

(a) providing an antibody as set forth in claim 100;

(b) providing a sample comprising polypeptides; and

(c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having a laccase activity.

104. A method of making an anti-laccase antibody comprising administering to a non-human animal a nucleic acid as set forth in claim 1 or claim 24 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-laccase antibody.

105. A method of making an anti-laccase antibody comprising administering to a non-human animal a polypeptide as set forth in claim 60 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-laccase antibody.

106. A method of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid comprises a sequence as set forth in claim 1 or claim 24; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide.

107. The method of claim 106, further comprising transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide.

108. A method for identifying a polypeptide having a laccase activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a laccase substrate; and

(c) contacting the polypeptide with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a laccase activity.

109. A method for identifying a laccase substrate comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a test substrate; and

(c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as a laccase substrate.

110. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

(a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid has a sequence as set forth in claim 1 or claim 24;

(b) providing a test compound;

(c) contacting the polypeptide with the test compound; and

(d) determining whether the test compound of step (b) specifically binds to the polypeptide.

111. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

(a) providing a polypeptide as set forth in claim 60;

(b) providing a test compound;

(c) contacting the polypeptide with the test compound; and

(d) determining whether the test compound of step (b) specifically binds to the polypeptide.

112. A method for identifying a modulator of a laccase activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a test compound;

(c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the laccase, wherein a change in the laccase activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the laccase activity.

113. The method of claim 112, wherein the laccase activity is measured by providing a laccase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product.

114. The method of claim 113, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of a laccase activity.

115. The method of claim 113, wherein an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of a laccase activity.

116. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises sequence as set forth in claim 60, a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

117. The computer system of claim 115, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

118. The computer system of claim 117, wherein the sequence comparison algorithm comprises a computer program that indicates polymorphisms.

119. The computer system of claim 117, further comprising an identifier that identifies one or more features in said sequence.

120. A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

121. A method for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and (b) identifying one or more features in the sequence with the computer program.

122. A method for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60 or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and (b) determining differences between the first sequence and the second sequence with the computer program.

123. The method of claim 122, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

124. The method of claim 123, further comprising an identifier that identifies one or more features in a sequence.

125. The method of claim 124, comprising reading the first sequence using a computer program and identifying one or more features in the sequence.

126. A method for isolating or recovering a nucleic acid encoding a polypeptide with a laccase activity from an environmental sample comprising the steps of:

(a) providing an amplification primer sequence pair as set forth in claim 31 or claim 33;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide with a laccase activity from an environmental sample.

127. The method of claim 126, wherein each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID NO:25, or a subsequence thereof.

128. A method for isolating or recovering a nucleic acid encoding a polypeptide with a laccase activity from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe comprising a sequence as set forth in claim 1 or claim 24, or a subsequence thereof;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a laccase activity from an environmental sample.

129. The method of claim 127 or claim 128, wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample.

130. The method of claim 129, wherein the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

131. A method of generating a variant of a nucleic acid encoding a polypeptide with a laccase activity comprising the steps of:

(a) providing a template nucleic acid comprising a sequence as set forth in claim 1 or claim 24; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid.

132. The method of claim 131, further comprising expressing the variant nucleic acid to generate a variant laccase polypeptide.

133. The method of claim 131, wherein the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis™ (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

134. The method of claim 131, wherein the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence

recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

135. The method of claim 131, wherein the method is iteratively repeated until a laccase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced.

136. The method of claim 135, wherein the variant laccase polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature.

137. The method of claim 135, wherein the variant laccase polypeptide has increased glycosylation as compared to the laccase encoded by a template nucleic acid.

138. The method of claim 135, wherein the variant laccase polypeptide has a laccase activity under a high temperature, wherein the laccase encoded by the template nucleic acid is not active under the high temperature.

139. The method of claim 131, wherein the method is iteratively repeated until a laccase coding sequence having an altered codon usage from that of the template nucleic acid is produced.

140. The method of claim 131, wherein the method is iteratively repeated until a laccase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

141. A method for modifying codons in a nucleic acid encoding a polypeptide with a laccase activity to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a laccase activity comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

142. A method for modifying codons in a nucleic acid encoding a laccase polypeptide, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a laccase activity comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a laccase.

143. A method for modifying codons in a nucleic acid encoding a laccase polypeptide to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a laccase polypeptide comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

144. A method for modifying a codon in a nucleic acid encoding a polypeptide having a laccase activity to decrease its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a laccase polypeptide comprising a sequence as set forth in claim 1 or claim 24; and

(b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell.

145. The method of claim 144, wherein the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

146. A method for producing a library of nucleic acids encoding a plurality of modified laccase active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 or SEQ ID NO:25, or a subsequence thereof, and the nucleic acid encodes a laccase active site or a laccase substrate binding site;

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified laccase active sites or substrate binding sites.

147. The method of claim 145, comprising mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, Gene Site Saturation Mutagenesis™ (GSSM), or a synthetic ligation reassembly (SLR).

148. The method of claim 145, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis™ (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

149. The method of claim 145, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

150. A method for making a small molecule comprising the following steps:

(a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises a laccase enzyme encoded by a nucleic acid comprising a sequence as set forth in claim 1 or claim 24;

(b) providing a substrate for at least one of the enzymes of step (a); and

(c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

151. A method for modifying a small molecule comprising the following steps:

(a) providing a laccase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence as set forth in claim 1 or claim 24;

(b) providing a small molecule; and

(c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the laccase enzyme, thereby modifying a small molecule by a laccase enzymatic reaction.

152. The method of claim 151, comprising a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the laccase enzyme.

153. The method of claim 151, further comprising a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions.

154. The method of claim 153, further comprising the step of testing the library to determine if a particular modified small molecule which exhibits a desired activity is present within the library.

155. The method of claim 154, wherein the step of testing the library further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

156. A method for determining a functional fragment of a laccase enzyme comprising the steps of:

(a) providing a laccase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and

(b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a laccase activity, thereby determining a functional fragment of a laccase enzyme.

157. The method of claim 156, wherein the laccase activity is measured by providing a laccase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

158. A method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps:

(a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid comprising a sequence as set forth in claim 1 or claim 24;

(b) culturing the modified cell to generate a plurality of modified cells;

(c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and,

(d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis.

159. The method of claim 158, wherein the genetic composition of the cell is modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene.

160. The method of claim 158, further comprising selecting a cell comprising a newly engineered phenotype.

161. The method of claim 160, further comprising culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

162. An isolated or recombinant signal sequence consisting of a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43, 1 to 44, 1 to 45, 1 to 46, or 1 to 47, of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID

NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26; or, consisting of a signal sequence as set forth in Table 1.

163. A chimeric polypeptide comprising at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 162, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

164. The chimeric polypeptide of claim 163, wherein the heterologous polypeptide or peptide is not a laccase.

165. The chimeric polypeptide of claim 163, wherein the heterologous polypeptide or peptide is amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP) or a laccase catalytic domain (CD).

166. An isolated or recombinant nucleic acid encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 162 and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

167. A method of increasing thermotolerance or thermostability of a laccase polypeptide, the method comprising glycosylating a laccase, wherein the polypeptide comprises at least thirty contiguous amino acids of a polypeptide as set forth in claim 60, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24, thereby increasing the thermotolerance or thermostability of the laccase.

168. A method for overexpressing a recombinant laccase in a cell comprising expressing a vector comprising a nucleic acid sequence as set forth in claim 1 or claim 24, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

169. A method of making a transgenic plant comprising the following steps:

(a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 24, thereby producing a transformed plant cell;

(b) producing a transgenic plant from the transformed cell.

170. The method as set forth in claim 169, wherein the step (a) further comprises introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts.

171. The method as set forth in claim 169, wherein the step (a) comprises introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment or by using an *Agrobacterium tumefaciens* host.

172. A method of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps:

(a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 24;

(b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

173. A method for hydrolyzing, breaking up or disrupting a lignin-comprising composition comprising the following steps:

(a) providing a polypeptide having a laccase activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

(b) providing a composition comprising a lignin; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the laccase hydrolyzes, breaks up or disrupts the lignin-comprising composition.

174. The method as set forth in claim 173, wherein the composition comprises a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell.

175. A dough or a bread product comprising a polypeptide as set forth in claim 64.

176. A method of dough conditioning comprising contacting a dough or a bread product with at least one polypeptide as set forth in claim 64 under conditions sufficient for conditioning the dough.

177. A beverage comprising a polypeptide as set forth in claim 64.

178. A method of beverage production comprising administration of at least one polypeptide as set forth in claim 64 to a beverage or a beverage precursor under conditions sufficient for decreasing the viscosity of the beverage.

179. The method of claim 178, wherein the beverage or beverage precursor is a wort or a beer.

180. A food, a feed or a nutritional supplement comprising a polypeptide as set forth in claim 64.

181. A method for utilizing a laccase as a nutritional supplement in an animal diet, the method comprising:

preparing a nutritional supplement containing a laccase enzyme comprising at least thirty contiguous amino acids of a polypeptide as set forth in claim 64; and

administering the nutritional supplement to an animal to increase utilization of a feed or a food ingested by the animal.

182. The method of claim 181, wherein the animal is a human.

183. The method of claim 181, wherein the animal is a human.

184. The method of claim 181, wherein the animal is a ruminant or a monogastric animal.

185. The method of claim 181, wherein the laccase enzyme is prepared by expression of a polynucleotide encoding the laccase in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal.

186. The method of claim 185, wherein the organism is selected from the group consisting of a *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

187. An edible enzyme delivery matrix comprising a thermostable recombinant laccase enzyme.

188. The edible enzyme delivery matrix of claim 187 comprising a polypeptide as set forth in claim 64.

189. A method for delivering a laccase supplement to an animal, the method comprising:

preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and a thermostable recombinant laccase enzyme, wherein the pellets readily disperse the laccase enzyme contained therein into aqueous media, and

administering the edible enzyme delivery matrix to the animal.

190. The method of claim 189, wherein the recombinant laccase enzyme comprises a polypeptide as set forth in claim 64.

191. The method of claim 189, wherein the granulate edible carrier. comprises a carrier selected from the group consisting of a grain germ, a grain germ that is spent of oil, a hay, an alfalfa, a timothy, a soy hull, a sunflower seed meal and a wheat midd.

192. The method of claim 189, wherein the edible carrier comprises grain germ that is spent of oil.

193. The method of claim 189, wherein the laccase enzyme is glycosylated to provide thermostability at pelletizing conditions.

194. The method of claim 189, wherein the delivery matrix is formed by pelletizing a mixture comprising a grain germ and a laccase.

195. The method of claim 189, wherein the pelletizing conditions include application of steam.

196. The method of claim 189, wherein the pelletizing conditions comprise application of a temperature in excess of about 80°C for about 5 minutes and the enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

197. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having a laccase activity and a signal sequence, wherein the nucleic acid comprises a sequence as set forth in claim 1.

198. The isolated or recombinant nucleic acid of claim 197, wherein the signal sequence is derived from another laccase or a non-laccase enzyme.

199. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having a laccase activity, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence as set forth in claim 1.

200. A cellulose- or cellulose derivative- composition comprising a polypeptide as set forth in claim 64.

201. A wood, wood pulp or wood product comprising a polypeptide as set forth in claim 64.

202. A paper, paper pulp or paper product comprising a polypeptide as set forth in claim 64.

203. A method for reducing lignin in a paper, a wood or wood product comprising contacting the paper, wood or wood product with a polypeptide as set forth in claim 64.

204. A detergent composition comprising a polypeptide as set forth in claim 64.

205. A pharmaceutical composition comprising a polypeptide as set forth in claim 64.

206. The pharmaceutical composition of claim 205 formulated in a topical delivery agent.

207. The pharmaceutical composition of claim 206, wherein the formulation comprises a lotion, a spray or a gel.

208. A method for eliminating or protecting animals from a microorganism comprising a lignin comprising administering a polypeptide as set forth in claim 64.

209. The method of claim 208, wherein the microorganism is a bacterium.

210. The method of claim 209, wherein the bacterium is a salmonellae.

211. A method for treatment and/or preventing a dermatitis comprising administering an effective amount of a polypeptide as set forth in claim 64.

212. The method of claim 211, wherein the dermatitis is a poison ivy dermatitis.

213. The method of claim 211, wherein the laccase is an oxidase.

214. The method of claim 214, wherein the oxidase is a para-diphenol oxidase.

215. A dairy product comprising a polypeptide as set forth in claim 64.

216. The dairy product of claim 213 comprising a milk, an ice cream, a cheese or a yogurt.

217. A method for improving texture and flavor of a dairy product comprising the following steps: (a) providing a polypeptide of the invention as set forth in claim 64; (b) providing a dairy product; and (c) contacting the polypeptide of step (a) and the dairy product of step (b) under conditions wherein the laccase can improve the texture or flavor of the dairy product.

218. A tobacco product comprising a polypeptide as set forth in claim 64.

219. The tobacco product of claim 218 comprising a cigarette, a cigar, pipe tobacco, a chewing tobacco.

220. A method for making tobacco products having a reduced amount of phenolic compounds comprising the following steps: (a) providing a polypeptide as set forth in claim 64; (b) providing a tobacco product; and (c) contacting the polypeptide of step (a) and the tobacco product of step (b) under conditions wherein the laccase can reduce the amount of phenolic compounds in the tobacco product.

221. The method of claim 220, wherein the laccase has a phenol oxidizing activity.

222. The method of claim 220, further comprising the step of removing the oxidized phenolic compound.

223. The method of claim 220, further comprising the step of removing and/or inactivating the laccase.

224. A composition comprising a surface comprising a polypeptide as set forth in claim 64.

225. The composition of claim 224, wherein the composition is a medical device or instrument, a medical implant or catheter, a surgical device or a dressing.

226. A method for cleaning or disinfecting a composition comprising the following steps: (a) providing a polypeptide as set forth in claim 64; (b) providing a composition; and (c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the laccase can clean or disinfect the composition.

227. A method for reducing oxygen gas in a confined space or compartment comprising treating a gas in a confined space or compartment with a polypeptide as set forth in claim 64.

228. A method for producing a nootkatone, comprising reacting valencene at a concentration of at least about 0.1% (v/v) and a composition having a laccase activity at temperature anywhere in the range of between about 4°C to about 75°C in the presence of an oxygen source.

229. The method of claim 228, further comprising recovering nootkatone from the reaction.

230. The method of claim 228, wherein the composition having laccase activity comprises a polypeptide as set forth in claim 64.

231. The method of claim 228, wherein valencene and the composition having laccase activity are reacted in the presence of a catalyst or an additional protein.

232. The method of claim 231, wherein the catalyst is selected from the group consisting of iron, ascorbic acid, cobalt, copper and combinations thereof.

233. The method of claim 228, wherein valencene and the composition having a laccase activity are reacted in the presence of a mediator.

234. The method of claim 233, wherein the mediator comprises 2,2-azinobis-(3-ethylbenzthiazoline-6-sulfonate) (ABTS), 1- hydroxybenzotriazole (HBT), 2,2,6,6-tetramethylpiperidin-1-yloxy (TEMPO), dimethoxyphenol, dihydroxyfumaric acid (DHF), 1-hydroxybenzotriazole (HBT), N-benzoyl-N-phenyl hydroxylamine (BPHA), N-hydroxyphthalimide, 3-hydroxy-1,2,3-benzotriazin-4-one, promazine, 1,8-Dihydroxy-4,5-dinitroanthraquinone, phenoxazine, anthraquinone, 2-hydroxy-1,4-naphthoquinone, phenothiazine, syringaldazine, anthrone, anthracene, anthrarufin, anthrarobin, 2,2'-azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) (ABTS), dimethoxyphenol (DMP), ferulic acid, catechin, epicatechin, homovanillic acid (HMV) or 2,3-dihydroxybenzoic acid (2,3-DHB) or combinations thereof.

235. The method of claim 228, wherein temperature anywhere in the range of between about 30°C to about 45°C.

236. The method of claim 228, wherein the reaction is done at a pH anywhere in the range of between about pH 3.0 to about pH 10.0.

237. The method of claim 228, wherein the oxygen source is selected from the group consisting of a mixed gas and pure oxygen.

238. The method of claim 228, wherein the composition having laccase activity comprises a protein having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 or SEQ ID NO:26.

239. The method of claim 231, wherein the catalyst or additional protein comprises a catalyst or a protein comprising a horse-radish peroxidase, a lactoperoxidase, a chloroperoxidase, a lignin peroxidase, a soybean peroxidase and/or a manganese peroxidase or combinations thereof.

240. A method of producing a nootkatone, comprising providing a polypeptide as set forth in claim 64, contacting a valencene with the polypeptide to produce the nootkatone.

241. The method of claim 240, wherein the nootkatone comprises a (-)-(4S,4aR,6S)-nootkatone.

242. The method of claim 240, wherein the nootkatone comprises a (+)-(4R,4aS,6R)-nootkatone.

243. The method of claim 240, wherein valencene is contacted by the protein at a temperature anywhere in the range of between about 4°C to 75°C.

244. The method of claim 240, wherein valencene is contacted by the protein in the presence of a catalyst or an additional protein.

245. The method of claim 244, wherein the catalyst comprises an iron, an ascorbic acid, a cobalt and/or a copper or combinations thereof.

246. The method of claim 244, wherein the catalyst or additional protein comprises a catalyst or a protein comprising a horse-radish peroxidase, a lactoperoxidase, a chloroperoxidase, a lignin peroxidase, a soybean peroxidase and/or a manganese peroxidase or combinations thereof.

247. The method of claim 240, further comprising contacting the valencene with the polypeptide in the presence of a mediator.

248. The method of claim 247, wherein the mediator acts as the catalyst.

249. The method of claim 247, wherein the mediator comprises 2,2-azinobis-(3-ethylbenzthiazoline-6-sulfonate) (ABTS), 1- hydroxybenzotriazole (HBT), 2,2,6,6-tetramethylpiperidin-1-yloxy (TEMPO), dimethoxyphenol, dihydroxyfumaric acid (DHF), 1-hydroxybenzotriazole (HBT), N-benzoyl-N-phenyl hydroxylamine (BPHA), N-hydroxyphthalimide, 3-hydroxy-1,2,3-benzotriazin-4-one, promazine, 1,8-

Dihydroxy-4,5-dinitroanthraquinone, phenoxazine, anthraquinone, 2-hydroxy-1,4-naphthoquinone, phenothiazine, syringaldazine, anthrone, anthracene, anthrarufin, anthrarobin, 2,2'-azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) (ABTS), dimethoxyphenol (DMP), ferulic acid, catechin, epicatechin, homovanillic acid (HMV) and/or 2,3-dihydroxybenzoic acid (2,3-DHB) or combinations thereof.

250. The method of claim 240, wherein the valencene is contacted by the protein at a pH anywhere in the range of between about pH 3.0 to about pH 10.0.

251. The method of claim 240, wherein valencene is present at a concentration of at least about 0.1 % (v/v).

252. The method of claim 243, wherein valencene is contacted by the protein anywhere in the range of between about 30°C to 45°C.

253. A composition comprising a nootkatone made by the method of claim 228 or claim 240.

254. A method of producing nootkatone, comprising contacting valencene with a mediator which has been oxidized or activated by contacting a protein having laccase activity to produce nootkatone, and recovering the produced nootkatone.

255. The method of claim 254, wherein valencene and the composition having laccase activity are reacted in the presence of a catalyst or an additional protein.

256. The method of claim 255, wherein the catalyst is selected from the group consisting of iron, ascorbic acid, cobalt, copper and combinations thereof.

257. The method of claim 254, wherein valencene and the composition having laccase activity are reacted in the presence of a mediator.

258. The method of claim 257, wherein the mediator comprises 2,2-azinobis-(3-ethylbenzthiazoline-6-sulfonate) (ABTS), 1- hydroxybenzotriazole (HBT),

2,2,6,6-tetramethylpiperidin-1-yloxy (TEMPO), dimethoxyphenol, dihydroxyfumaric acid (DHF), 1-hydroxybenzotriazole (HBT), N-benzoyl-N-phenyl hydroxylamine (BPHA), N-hydroxyphthalimide, 3-Hydroxy-1,2,3-benzotriazin-4-one, promazine, 1,8-Dihydroxy-4,5-dinitroanthraquinone, phenoxazine, anthraquinone, 2-hydroxy-1,4-naphthoquinone, phenothiazine, syringaldazine, anthrone, anthracene, anthrarufin, anthrarobin, 2,2'-azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) (ABTS), dimethoxyphenol (DMP), ferulic acid, catechin, epicatechin, homovanillic acid (HMV) and/or 2,3-dihydroxybenzoic acid (2,3-DHB) or combinations thereof.

259. The method as claim 107, wherein the host is selected from the group consisting of a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell.

260. The method of claim 259, wherein the host is selected from the group consisting of a *Schizosaccharomyces* sp., *Saccharomyces* sp., *Pichia* sp., *Escherichia* sp., *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

261. The method of claim 260, wherein the organism is *S. pombe*.

262. The method of claim 260, wherein the organism is *S. cerevisiae*.

263. The method of claim 260, wherein the organism is *P. pastoris*.

264. The method of claim 260, wherein the organism is *E. coli*.

265. The method of claim 260, wherein the organism is *Bacillus cereus*.